OIPE

RAW SEQUENCE LISTING DATE: 01/29/2002
PATENT APPLICATION: US/09/929,313 TIME: 10:34:57

Input Set : N:\Crf3\RULE60\09929313.raw
Output Set: N:\CRF3\01292002\I929313.raw


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1 <110> APPLICANT: Kao, Hung-Teh
2       Hartig, Paul R.
3       Branchek, Theresa
4 <120> TITLE OF INVENTION: DNA Encoding A Human Serotonin (5-HT2) Receptor and
5       Uses Thereof
6 <130> FILE REFERENCE: 35997a3zy/JPW
8 <140> CURRENT APPLICATION NUMBER: 09/929,313
9 <141> CURRENT FILING DATE: 2001-08-14
11 <150> PRIOR APPLICATION NUMBER: US/09/145,864
12 <151> PRIOR FILING DATE: 1998-09-02
14 <160> NUMBER OF SEQ ID NOS: 4
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1483
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(1440)
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26      Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
27        1               5                  10                  15
28      tcc cta atg caa tta aat gat gac acc agg ctc tac agt aat gac ttt   96
29      Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
30                  20                  25                  30
31      aac tcc gga gaa gct aac act tct gat gca ttt aac tgg aca gtc gac   144
32      Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
33              35                  40                  45
34      tct gaa aat cga acc aac ctt tcc tgt gaa ggg tgc ctc tca ccg tcg   192
35      Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
36           50                  55                  60
37      tgt ctc tcc tta ctt cat ctc cag gaa aaa aac tgg tct gct tta ctg   240
38      Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
39       65                  70                  75                  80
40      aca gcc gta gtg att att cta act att gct gga aac ata ctc gtc atc   288
41      Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
42                      85                  90                  95
43      atg gca gtg tcc cta gag aaa aag ctg cag aat gcc acc aac tat ttc   336
44      Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
45                  100                 105                 110
46      ctg atg tca ctt gcc ata gct gat atg ctg ctg ggt ttc ctt gtc atg   384
47      Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
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48                 115                 120                 125
49      ccc gtg tcc atg tta acc atc ctg tat ggg tac cgg tgg cct ctg ccg   432
50      Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
51          130                 135                 140
52      agc aag ctt tgt gca gtc tgg att tac ctg gac gtg ctc ttc tcc acg   480
53      Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
54      145                 150                 155                 160
55      gcc tcc atc atg cac ctc tgc gcc atc tcg ctg gac cgc tac gtc gcc   528
56      Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
57                      165                 170                 175
58      atc cag aat ccc atc cac cac agc cgc ttc aac tcc aga act aag gca   576
59      Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
60                  180                 185                 190
61      ttt ctg aaa atc att gct gtt tgg acc ata tca gta ggt ata tcc atg   624
62      Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
63              195                 200                 205
64      cca ata cca gtc ttt ggg cta cag gac gat tcg aag gtc ttt aag gag   672
65      Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
66          210                 215                 220
67      ggg agt tgc tta ctt gcc gat gat aac ttt gtc ctg atc ggc tct ttt   720
68      Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
69      225                 230                 235                 240
70      gtg tca ttt ttc att ccc tta acc atc atg gtg atc acc tac ttt cta   768
71      Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
72                      245                 250                 255
73      act atc aag tca ctc cag aaa gaa gct act ttg tgt gta agt gat ctt   816
74      Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
75                  260                 265                 270
76      ggc aca cgg gcc aaa tta gct tct ttc agc ttc ctc cct cag agt tct   864
77      Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
78              275                 280                 285
79      ttg tct tca gaa aag ctc ttc cag cgg tcg atc cat agg gag cca ggg   912
80      Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
81          290                 295                 300
82      tcc tac aca ggc agg agg act atg cag tcc atc agc aat gag caa aag   960
83      Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
84      305                 310                 315                 320
85      gca tgc aag gtg ctg ggc atc gtc ttc ttc ctg ttt gtg gtg atg tgg   1008
86      Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
87                      325                 330                 335
88      tgc cct ttc ttc atc aca aac atc atg gcc gtc atc tgc aaa gag tcc   1056
89      Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
90                  340                 345                 350
91      tgc aat gag gat gtc att ggg gcc ctg ctc aat gtg ttt gtt tgg atc   1104
92      Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
93              355                 360                 365
94      ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac   1152
95      Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
96          370                 375                 380
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Input Set : N:\Crf3\RULE60\09929313.raw
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 97       aag acc tat agg tca gcc ttt tca cgg tat att cag tgt cag tac aag   1200
 98       Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
 99       385                 390                 395                 400
100        gaa aac aaa aaa cca ttg cag tta att tta gtg aac aca ata ccg gct   1248
101        Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
102                        405                 410                 415
103        ttg gcc tac aag tct agc caa ctt caa atg gga caa aaa aag aat tca   1296
104        Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
105                    420                 425                 430
106        aag caa gat gcc aag aca aca gat aat gac tgc tca atg gtt gct cta   1344
107        Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
108                435                 440                 445
109        gga aag cag cat tct gaa gag gct tct aaa gac aat agc gac gga gtg   1392
110        Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
111            450                 455                 460
112        aat gaa aag gtg agc tgt gtg tga tag gct agt tgc cgt ggc aac tgt   1440
113        Asn Glu Lys Val Ser Cys Val         Ala Ser Cys Arg Gly Asn Cys
W--> 114   465                 470                 475                 480
115        ggaaggcaca ctgagcaagt tttcacctat ctggtttttt ttg                  1483
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 471
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
121 <400> SEQUENCE: 2
122        Met Asp Ile Leu Cys Glu Glu Asn Thr Ser Leu Ser Ser Thr Thr Asn
123          1               5                  10                  15
124        Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
125                      20                  25                  30
126        Asn Ser Gly Glu Ala Asn Thr Ser Asp Ala Phe Asn Trp Thr Val Asp
127                  35                  40                  45
128        Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
129                50                  55                  60
130        Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
131        65                  70                  75                  80
132        Thr Ala Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
133                        85                  90                  95
134        Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
135                    100                 105                 110
136        Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
137                115                 120                 125
138        Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
139            130                 135                 140
140        Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
141        145                 150                 155                 160
142        Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
143                        165                 170                 175
144        Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
145                    180                 185                 190
146        Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
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147                 195                 200                 205
148     Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
149         210                 215                 220
150     Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
151     225                 230                 235                 240
152     Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
153                     245                 250                 255
154     Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
155                 260                 265                 270
156     Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
157             275                 280                 285
158     Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
159         290                 295                 300
160     Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
161     305                 310                 315                 320
162     Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
163                     325                 330                 335
164     Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
165                 340                 345                 350
166     Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
167             355                 360                 365
168     Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
169         370                 375                 380
170     Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
171     385                 390                 395                 400
172     Glu Asn Lys Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
173                     405                 410                 415
174     Leu Ala Tyr Lys Ser Ser Gln Leu Gln Met Gly Gln Lys Lys Asn Ser
175                 420                 425                 430
176     Lys Gln Asp Ala Lys Thr Thr Asp Asn Asp Cys Ser Met Val Ala Leu
177             435                 440                 445
178     Gly Lys Gln His Ser Glu Glu Ala Ser Lys Asp Asn Ser Asp Gly Val
179         450                 455                 460
180     Asn Glu Lys Val Ser Cys Val
181     465                 470
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184 <211> LENGTH: 7
185 <212> TYPE: PRT
186 <213> ORGANISM: Homo sapiens
187 <400> SEQUENCE: 3
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194 <213> ORGANISM: Rattus norvegicus
195 <400> SEQUENCE: 4
196       Met Glu Ile Leu Cys Glu Asp Met Ile Ser Leu Ser Ser Ile Pro Met
197         1               5                   10                  15
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Ser Leu Met Asp Leu Gly Asp Gly Pro Ala Leu Val His Asn Asp Phe
                20                  25                  30
Asn Ser Arg Asp Ala Asn Thr Ser Glu Ala Ser Asn Trp Thr Ile Asp
            35                  40                  45
Ala Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Tyr Leu Pro Pro Thr
        50                  55                  60
Cys Leu Ser Ile Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
65                  70                  75                  80
Thr Thr Val Val Ile Ile Leu Thr Ile Ala Gly Asn Ile Leu Val Ile
                85                  90                  95
Met Ala Val Ser Leu Glu Lys Lys Leu Gln Asn Ala Thr Asn Tyr Phe
            100                 105                 110
Leu Met Ser Leu Ala Ile Ala Asp Met Leu Leu Gly Phe Leu Val Met
        115                 120                 125
Pro Val Ser Met Leu Thr Ile Leu Tyr Gly Tyr Arg Trp Pro Leu Pro
    130                 135                 140
Ser Lys Leu Cys Ala Ile Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr
145                 150                 155                 160
Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala
                165                 170                 175
Ile Gln Asn Pro Ile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala
            180                 185                 190
Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met
        195                 200                 205
Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu
    210                 215                 220
Gly Ser Cys Leu Leu Ala Asp Asp Asn Phe Val Leu Ile Gly Ser Phe
225                 230                 235                 240
Val Ala Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu
                245                 250                 255
Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu
            260                 265                 270
Ser Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser
        275                 280                 285
Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly
    290                 295                 300
Ser Tyr Ala Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys
305                 310                 315                 320
Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp
                325                 330                 335
Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser
            340                 345                 350
Cys Asn Glu Asn Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile
        355                 360                 365
Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn
    370                 375                 380
Lys Thr Tyr Arg Ser Ala Phe Ser Arg Tyr Ile Gln Cys Gln Tyr Lys
385                 390                 395                 400
Glu Asn Arg Lys Pro Leu Gln Leu Ile Leu Val Asn Thr Ile Pro Ala
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VERIFICATION SUMMARY DATE: 01/29/2002
PATENT APPLICATION: US/09/929,313 TIME: 10:34:58

Input Set : N:\Crf3\RULE60\09929313.raw
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L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1